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EXAMINER	
BAUSCH, SARAE L	

ART UNIT	PAPER NUMBER
1634	

DATE MAILED: 07/27/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No. 10/009,340	Applicant(s) DUBREUCQ ET AL.
	Examiner Sarae Bausch	Art Unit 1634

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *05 May 2005*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-24* is/are pending in the application.

4a) Of the above claim(s) *7-24* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-6* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☒ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☒ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *03/02*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

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DETAILED ACTION

The examiner reviewing your application at the PTO has changed. To aid in correlating any papers for this application, all further correspondence regarding this application should be directed to examiner Sarae Bausch.

Election/Restrictions

1. Applicant's election with traverse of group I, claims 1-6, in the reply filed on 05/05/2005 is acknowledged. The traversal is on the ground(s) that the claims do possess unity of invention and there is no undue burden to search all of the claims. This is not found persuasive because as stated in the restriction requirement on page 2, mailed 02/01/2005, the inventions are linked by the technical feature of a promoter which expresses in all plant tissues except dry or mature seeds and has at least 80% sequence identity with any portion of any length of an Arabidopsis FAH promoter. Furthermore, the previous office action stated that the feature was not special because it does not constitute an advance over the prior art and therefore lacks unity of invention. For these reasons and the reasons made of record in the previous office action, the restriction requirement is maintained.

The requirement is still deemed proper and is therefore made FINAL.

2. Claims 7-24 are withdrawn from further consideration pursuant to 37 CFR 1.142(b), as being drawn to a nonelected invention, there being no allowable generic or linking claim. Applicant timely traversed the restriction (election) requirement in the reply filed on 05/05/2005.

Claim Rejections - 35 USC § 101

3. 35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

Claims 1-3 and 5-6 are rejected under 35 U.S.C. 101 because the claimed invention is directed to non-statutory subject matter. The claims encompass a promoter sequence which allows the expression of a gene of interest in the tissues of a plant, however the claim is not drawn to an isolated promoter sequence and therefore reads on a product of nature. As stated in the MPEP, section 2105 [R-1], "the test set down by the Court for patentable subject matter in this area is whether the living matter is the result of human intervention." In the instant claims, the claims are broadly drawn to a product of nature and as such are not the result of human intervention and therefore are non-statutory subject matter.

Claim Rejections - 35 USC § 112- Second Paragraph

4. The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

5. Claims 4 and 6 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

(a) Claim 4 is indefinite for the recitation of "accessible under the number AC003096" because it is not clear what "AC003096" means. This is an arbitrary identifier utilized in the claims and the specification. Applicants appear to be referring to a record in a biological database, however there are many different databases (GenBank, PubMed, OMIM, dbSNP, etc.) and the database in question is not identified in the specification or the claims. Furthermore, if applicant intends to be referring, for example, to GenBank accession number AC003096, this reference is indefinite as well because the sequence in this record has had at least eight different versions prior to 02/27/2002, and it is not clear which one applicant is referring to. In each

version of the sequence, the sequence is potentially different and so the context to which applicant is referring is unclear.

(b) Claim 6 provides for the use of a sequence as claimed in claim 1, but, since the claim does not set forth any steps involved in the method/process, it is unclear what method/process applicant is intending to encompass. Claim 6 recites the use of a sequence as claimed in claim 1 for identifying fragments of the sequence SEQ ID No. 1, however the claim does not recite any active, positive steps delimiting how this use is actually practiced.

Claim 6 is rejected under 35 U.S.C. 101 because the claimed recitation of a use, without setting forth any steps involved in the process, results in an improper definition of a process, i.e., results in a claim which is not a proper process claim under 35 U.S.C. 101. See for example *Ex parte Dunki*, 153 USPQ 678 (Bd.App. 1967) and *Clinical Products, Ltd.* v. *Brenner*, 255 F. Supp. 131, 149 USPQ 475 (D.D.C. 1966). Claim 6 recites the use of a sequence as claimed in claim 1 for identifying fragments of the sequence of SEQ ID No. 1 but does not include any active, positive steps.

Claim Rejections - 35 USC § 112 – Written Description

6. The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

7. Claims 1-6 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant

art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Claim 1 and 5 are drawn to a promoter sequence that comprises a sequence having at least 80% identity with the sequence or a portion of the sequence of the promoter of the Arabidopsis FAH gene. While the specification asserts a protein of the fatty acid hydroxylase (FAH) type of Arabidopsis (see page 2, lines 36-38) and asserts Arabidopsis thaliana fatty hydroxylase as Fah1p (FAH1) (see page 5, lines 35-36), it does not however teach or describe all fatty acid hydroxylase genes that are associated with Arabidopsis thaliana. The claim is broadly drawn to any fatty acid hydroxylase from Arabidopsis thaliana and it appears from the teaching in the specification that FAH is a fatty acid hydroxylase type gene from Arabidopsis thaliana, however there are multiple fatty acidy hydroxylase type genes from Arabidopsis thaliana, Ruegger et al. (Plant Physiology, Jan 199, vol. 119, pp. 101-110) teaches that FAH1 is ferulate-5-hydroxylase (see abstract) is a fatty acid hydroxylase from Arabidopsis thaliana and Benveniste et al. (Biochemical and Biophysical Res. Comm. 243 (1998), pp. 688-693) teach CYP86A1 encodes a cytochrome P450-dependent fatty acid hydroxylase (see abstract). The prior art teaches two different fatty acid hydroxylases and the specification does not describe which FAH gene or protein is expressed using the claimed promoter.

With regard to claim 1 and 5, the recitation of comprising "a" sequence having at least 80% identity with the sequence or a portion of the sequence allows for nucleotides with altered sequence and substantial variation with regard to any promoter of any FAH gene of Arabidopsis and thus broadly encompasses variants, mutants, and fragments of any promoter from any source that are not described in the specification. The recitation of "a portion of the sequence"

broadly encompasses as few as two nucleotides of the promoter of any FAH gene of Arabidopsis from any source. Further, the recitation of "a" sequence encompasses a minimum of two nucleotides and broadly encompasses variants and fragments of the promoter of any FAH gene from Arabidopsis. Further, the specification does not disclose a single sequence with less than 100% identity to SEQ ID No. 1 with promoter activity. The specification does not disclose the critical regions of a sequence that would be 80% identical to SEQ ID No. 1 and still maintain promoter activity. The specification does not teach which sequences are essential, nonessential, and critical for promoter activity.

Claim 2 is drawn to a promoter sequence that comprises a sequence having at least 80% identity with the sequence or a portion of the sequence of the SEQ ID No. 1 (instant claim 2). While the specification does teach the sequence of SEQ ID No. 1, the recitation of comprising "a sequence having at least 80% identity with the sequence" allows for nucleotides with altered sequence and substantial variation with regard to SEQ ID No. 1 and thus broadly encompasses variants and fragments from any source that are not described in the specification. The recitation of "a portion of the sequence" broadly encompasses as few as two nucleotides of SEQ ID No. 1, as well as variants and fragments from any source. Further, the recitation of "a" sequence encompasses a minimum of two nucleotides and broadly encompasses variants and fragments of SEQ ID No. 1, which is not described or taught in the specification. Further, the specification does not disclose a single sequence with less than 100% identity to SEQ ID No. 1 with promoter activity. The specification does not disclose the critical regions of a sequence that would be 80% identical to SEQ ID No. 1 and still maintain promoter activity. The specification does not teach which sequences are essential, nonessential, and critical for promoter activity.

Claim 3 is drawn to a promoter sequence that comprises the sequence or "a portion of the sequence", SEQ ID No. 1. While the specification does teach the sequence of SEQ ID NO. 1, the recitation of "a portion of the sequence" broadly encompasses as few as two nucleotides of SEQ ID No. 1, as well as variants and fragments from any source, which is not described or taught in the specification. Further, the specification does not disclose a single sequence with less than 100% identity to SEQ ID No. 1 with promoter activity. The specification does not disclose the critical regions of a sequence that would be 80% identical to SEQ ID No. 1 and still maintain promoter activity. The specification does not teach which sequences are essential, nonessential, and critical for promoter activity.

Claim 4 is drawn to a method for isolating and characterizing the promoter of the FAH gene in plants using a primer comprising "a" sequence having at least 80% identity with a sequence containing at least 10 consecutive nucleotides of SEQ ID No. 5 or a complementary sequence or a primer which hybridizes under high stringency conditions to any coding sequence for SEQ ID No. 4 or a sequence having at least 80% identity with a sequence containing at least 10 consecutive nucleotides of the genomic sequence of FAH gene, accessible under AC003096 or a complementary sequence. While the specification does teach the sequence of SEQ ID No. 4 and SEQ ID No. 5, the recitation of "a" sequence having at least 80% identity broadly encompasses variants and fragments from any source, which is not described in the specification. Further, the recitation of "a complementary sequence" encompasses as few as two nucleotides of SEQ ID No. 4 or 5, as well as variants and fragments from any source which is not described in the specification. The recitation of "a primer which hybridizes under high stringency conditions to any coding sequence of SEQ ID No. 4" allows for polynucleotides with substantial variation

with regard to any coding sequence of SEQ ID No. 4. The specification does not teach high stringent conditions and this recitation does not connote structural limitations to the claims and as such it is not clear what resulting structure will occur from hybridization to the coding sequence of SEQ ID No. 4.

The claims are broadly drawn to any promoter sequence or portion of any promoter sequence for any fatty acid hydroxylase gene from Arabidopsis thaliana. The art teaches two different fatty acidy hydroxylase genes for Arabidopsis and that the acronym, FAH1 is used to abbreviate ferulate-5-hydroxylase from Arabidopsis but does not teach the acronym FAH. Ruegger et al. teach ferulate-5-hydroxylase (FAH1) is a fatty acid hydroxylase from Arabidopsis thaliana and Benveniste et al. (Biochemical and Biophysical Res. Comm. 243 (1998), pp. 688-693) teach CYP86A1 encodes a cytochrome P450-dependent fatty acid hydroxylase (see abstract). The specification does not disclose the critical regions of a sequence that would be 80% identical to SEQ ID No. 1 and still maintain promoter activity. The specification does not teach which sequences are essential, nonessential, and critical for promoter activity. The prior art teaches that mutations in a critical region of a promoter element can destroy the ability of a construct to function in promotion. Chan *et al.* (Plant Molecular Biology 46 :131-141, (2001)) mutation in a critical XXIII element of the GAPB promoter abolished transcription completely (Figure 6), while mutations in other elements did not abolish activity (Figure 6). However, the specification does not identify any region of the promoter sequence which is critical for promoter activity.

Thus, the scope of the claim includes numerous variants and fragments, and the genus is highly variant because a significant number of differences between genus members is

encompassed. Although the specification states that these types of changes are routinely done in the art, the specification and claims do not provide any guidance as to what changes should be made in order for the sequence to maintain promoter activity. The specification does not disclose a single sequence with less than 100% identity to SEQ ID No. 1 with promoter activity. The specification does not disclose what sequences are required and critical for promoter activity. The specification does identify a putative TATA box at –100 bp from the presumed transcription site and a CCAAT box at –190 bp from the transcription start site, however there are other functional regions within a promoter that are important for activity and the specification does not disclose any other region of the sequence that is essential for promoter activity. The specification does not disclose which portion or 80% identity of SEQ ID No. 1 is necessary for promoter activity.

The instant claims are drawn to undisclosed sequences with promoter activity that have not been contemplated. The specification provides insufficient written description to support the genus encompassed by the claim. Absent a written description, the specification fails to show that the applicant was "in possession of the claimed invention" at the time the application for the patent was filed. Further, the genus of polynucleotides comprised by the claim is a large variable genus, which can potentially encode proteins of diverse functions and read on genomic sequences. The specification only discloses a selected number of species of the genus; i.e. SEQ ID NO 1, 4, and 5, which is insufficient to put one of ordinary skill in the art in possession of all attributes and features of all species within the genus. Thus one skilled in the art cannot reasonably conclude that applicant had possession of the claimed invention at the time the instant application was filed with respect to claims 1-5. Additionally, claim 6 is dependent on claim 1.

Vas-Cath Inc. v. Mahurkar, 19 USPQ2d 1111, makes clear that "applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession *of the invention*. The invention is, for purposes of the 'written description' inquiry, *whatever is now claimed.*" (See page 1117.) The specification does not "clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed." (See *Vas-Cath* at page 1116.)

With the exception of SEQ ID NOS: 1, 4, and 5, the skilled artisan cannot envision the detailed chemical structure of the encompassed polynucleotides, regardless of the complexity or simplicity of the method of isolation. Adequate written description requires more than a mere statement that it is part of the invention and reference to a potential method for isolating it. The nucleic acid itself is required. See *Fiers v. Revel*, 25 USPQ2d 1601, 1606 (CAFC 1993), and *Amgen Inc. V. Chugai Pharmaceutical Co. Ltd.*, 18 USPQ2d 1016. In *Fiddes v. Baird*, 30 USPQ2d 1481, 1483, claims directed to mammalian FGF's were found unpatentable due to lack of written description for the broad class. The specification provided only the bovine sequence.

Finally, *University of California v. Eli Lilly and Co.*, 43 USPQ2d 1398, 1404, 1405 held that:

To fulfill the written description requirement, a patent specification must describe an invention and do so in sufficient detail that one skilled in the art can clearly conclude that "the inventor invented the claimed invention." *Lockwood v. American Airlines, Inc.*, 107 F.3d 1565, 1572, 41 USPQ2d 1961, 1966 (1997); In *re Gosteli*, 872 F.2d 1008, 1012, 10 USPQ2d 1614, 1618 (Fed. Cir. 1989) (" [T]he description must clearly allow persons of ordinary skill in the art to recognize that [the inventor] invented what is claimed."). Thus, an applicant complies with the written description requirement "by describing the invention, with all its claimed limitations, not that which makes it obvious," and by using "such descriptive means as words, structures, figures, diagrams, formulas, etc., that set forth the claimed invention." *Lockwood*, 107 F.3d at 1572, 41 USPQ2d at 1966.

An adequate written description of a DNA, such as the cDNA of the recombinant plasmids and microorganisms of the '525 patent, "requires a precise definition, such as by structure, formula, chemical name, or physical properties," not a mere wish or plan for obtaining the claimed chemical invention. *Fiers v. Revel*, 984 F.2d 1164, 1171, 25 USPQ2d 1601, 1606 (Fed. Cir. 1993). Accordingly, "an adequate written description of a DNA requires more than a mere statement that it is part of the invention and reference to a potential method for isolating it; what is required is a description of the DNA itself." Id. at 1170, 25 USPQ2d at 1606.

Claim Rejections - 35 USC § 112- Enablement

8. The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

9. Claims 1-6 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

Factors to be considered in determining whether a disclosure meets the enablement requirement of 35 USC 112, first paragraph, have been described by the court in *In re Wands*, 8 USPQ2d 1400 (CA FC 1988). *Wands* states at page 1404,

> "Factors to be considered in determining whether a disclosure would require undue experimentation have been summarized by the board in Ex parte Forman. They include (1) the quantity of experimentation necessary, (2) the amount of direction or guidance presented, (3) the presence or absence of working examples, (4) the nature of the invention, (5) the state of the prior art, (6) the relative skill of those in the art, (7) the predictability or unpredictability of the art, and (8) the breadth of the claims."

<u>The nature of the invention and the breadth of the claims</u>

Claim 1 is broadly drawn to a promoter sequence that comprises a sequence having at least 80% identity with the sequence or a portion of the sequence of the promoter of "any" Arabidopsis FAH gene. Claims 2 and 3 are broadly drawn to a sequence that comprises at least

80% identity or a portion of the sequence of SEQ ID No. 1. Claim 4 is drawn to a method for isolating and characterizing the promoter of "any" FAH gene in plants. Claim 5 is broadly drawn to a promoter sequence that has at least 80% identity with the sequence or portion of the sequence of the promoter of FAH gene. Claim 6 is drawn to the use of a sequence that comprises a sequence having at least 80% identity with the sequence or a portion of the sequence of the promoter of Arabidopsis FAH gene. The claims are broadly drawn to promoter sequence that expresses the Arabidopsis fatty acidy hydroxylase gene, which includes variants, homologs, and mutations from any source of the promoter sequence for any fatty acid hydroxylase gene from Arabidopsis. The specification recites the identification of a promoter that allows strong expression of a transgene in all the tissues of the plants except the seed (see page 2, lines 10-15). However, as will be further discussed, the specification does not enable one of skill in the art to generate "any" promoter sequence comprising variants, mutants, or fragment of the promoter sequence of "any" FAH gene of Arabidopsis that is capable of expressing a gene of interest in the tissues of a plant except in the maturing seed and in the dry seed, as the specification does not teach what portion of the sequence is essential, nonessential and required for promoter activity.

Guidance in the Specification

While the specification does teach the sequence of a promoter, SEQ ID No. 1 and the gene expressed by this promoter, SEQ ID No. 5 and the protein that encodes the gene, SEQ ID No. 4, the specification provides no evidence of how to make or use mutants, variants, or homologs of SEQ ID No. 1 that are capable of functioning as a promoter to express any gene of interest in the tissues of a plant except in the maturing seed and in the dry seed. The specification merely discloses the sequence and structural information for the promoter encompassed in SEQ

ID No. 1 and recites that the invention relates to the use of a portion of the sequence SEQ ID No. 1 for identifying fragments capable of promoting the expression of a gene of interest in a plant except in the seed (page 5, lines 1-8). The specification recites that the promoter may be modified by adding sequence such as enhancers, and/or by deleting nonessential and/or undesired regions (see page 5, lines 5-11), however the specification gives no guidance as to what sequences can be added or deleted, what portion of the sequence is essential, nonessential or required for promoter activity. The specification does recite that using a primer comprising a sequence with 80% identity to SEQ ID No. 5 or a primer which hybridizes under high stringency condition can be used to isolate and characterize the promoter of the FAH gene in plants (see page 5, lines 15-30 and page 6, lines 15-25), however it does not teach which sequences or primers are necessary to isolate and characterize the promoter of the FAH gene. The specification does not teach the use of a promoter sequence that expresses Arabidopsis FAH gene to identify fragments of SEQ No. 1.

The unpredictability of the art and the state of the prior art

The ability of a promoter to function is highly sequence specific. The art teaches repeatedly that mutations in a critical region of a promoter element can destroy the ability of a construct to function in promotion. For example, Pietrzkowski *et al.* (Experimental Cell Research, 193, 283-290 (1991)) teaches that when synthetic promoters were produced wherein the sequence of an enhancer element was mutated, little to no promotion was observed from the constructs where the promoter was mutated (see for example Figure 6). Chan *et al.* (Plant Molecular Biology 46 :131-141, (2001)) mutation in a critical XXIII element of the GAPB promoter abolished transcription completely (Figure 6), while mutations in other elements did

not abolish activity (Figure 6). Thus, it is evident that it is highly unpredictable how promoter elements will respond to even very minor sequences changes. In addition, the order that promoter elements occur in a construct has an effect on the functionality of the promoter. Omilli *et al.* (Molecular and Cellular Biology, June 1986, p. 1875-1885) teach that the relative arrangement of promoter elements is a critical factor contributing to the activity of the promoter (ABSTRACT, for example).

Working Examples

On page 16, the specification provides an example of amplification of SEQ ID No. 1 by PCR using primers and identification of a putative TATA box at –100 bp from the presumed transcription site and a CCAAT box at –190 bp from the transcription start site. The specification describes cloning the PCR fragment into the construct pGEM-T vector and introducing this vector into a binary vector comprising the GUS reporter gene without a promoter and transforming the vector into planta (see page 16, lines 14-20). The specification asserts that there were thirteen primary transformant that were obtained and were tested for their GUS activity during development. The specification asserts that expression is strong from 20 hours after the start of soaking in the embryos and during development the expression is strong in all tissues (see page 16, lines 25-28). The specification asserts that these results demonstrate that the isolated promoter sequence indeed confers a very specific expression profile on the reporter gene used and the promoter is active throughout the development of the plant, in all tissues tested except in the seed of undergoing maturation (see page 16, lines 30-36). The specification asserts that the marker confirms functionality of the promoter and its specificity (see page 17, lines 1-2). However, the specification provides no control experiments of the

plasmid construct without a promoter sequence to determine of the GUS gene expression is due to the specific promoter.

Further, the specification provides no working examples of which portion of the promoter is necessary for expression of a gene. The specification is merely prophetic for determining the sequence of the promoter that is necessary for expression of a gene. The specification merely recites, on page 5, lines 1-10, that is may be possible to define the minimum region of the sequence of the promoter of the FAH gene for ensuring effective expression and the promoter may be modified by adding sequences such as enhancers and/or deletions of nonessential and/or undesirable regions. However, the specification does not give any guidance or working examples of which region of the promoter may be modified, deleted, or mutated and still maintain function as a promoter and specifically a promoter that is capable of expressing a gene in all tissues, except in the seed maturation. The specification envisions hypothetical situations where modification of the promoter sequence is possible without changing the function. However, it is unclear how one of skill in the art would design the most appropriate promoter sequence to practice this preferred embodiment of expressing a gene in all tissues, except in the seed maturation of a plant and furthermore, how one would determine the efficacy of the results of the embodiments as the specification does not teach a control experiment.

Level of Skill in the Art

The level of skill in the art is deemed to be high.

Quantity of Experimentation

Given the lack of guidance in the specification with regard to which sequences could be modified or which portion of the sequence of the promoter of SEQ ID No. 1 is required for promoter activity, the quantity of experimentation in this area is extremely large and undue. The skilled artisan would have to determine which nucleic acid residues, mutants, variants, and/or fragments would be capable of maintaining promoter activity and expressing a gene of interest in all tissues, except in the seed maturation of a plant. To practice the invention as broadly as it is claimed, the skilled artisan would have to construct and screen hundreds of millions of possible promoters that comprise encompasses variants, mutants, and homologs of SEQ ID NO 1 or any FAH gene from Arabidopsis, that would be capable of expressing a gene of interest in all tissue in a plant. The construction and screening of all of these possible promoters to determine the functional promoters would require undue experimentation because there is no way to predict which promoters would be functional given that promoter sequences are highly variable. The skilled artisan would have to perform an extremely large amount of trial and error analysis in a large study to determine if the promoter is in fact expressing a gene in all tissue except maturing seed and dry seed. This would require a large amount of inventive effort, with each of the many intervening steps, upon effective reduction to practice, not providing any guarantee of success in the succeeding steps. Thus given the broad claims in an art whose nature is identified as unpredictable, the lack of guidance on how to make a promoter that comprises mutants, variants, and homologs capable of expressing a gene of interest in all tissues of a plant except maturing seed and dry seed, the unpredictability of the art with regard to identifying sequences that are critical for promoter function, the large quantity of research required to define the lack of guidance provided in the specification, the absence of working examples, and the negative

teaching in the prior art balanced only against the high level of skill in the art, it is the position of the examiner that it would require undue experimentation for one of skill in the art to make the claimed invention.

Claim Rejections - 35 USC § 102

10. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

11. Claims 1-6 are rejected under 35 U.S.C. 102(b) as being anticipated by Mitchell et al. (J. Biological Chem. (1997) vol. 272, no. 45, pp. 28281-28288).

With regard to claim 1-3 and 6, Mitchell et al. teach a portion of the sequence of a promoter of the Arabidopsis FAH gene (see figure 4, page 28285). The claims broadly encompass a portion of the sequence of the promoter of the Arabidopsis FAH gene (fatty acid hydroxylase type). Therefore, the sequence of A. thaliana FAH1 as depicted in figure 4 by Mitchell et al. teach at least two nucleotides that encompass a portion of the sequence of the promoter of the Arabidopsis FAH gene. Further, the sequence in figure 4 of FAH1 open reading frame taught by Mitchell et al. encompass a fragment of SEQ ID No. 1 (instant claim 6).

With regard to claim 4 and 5, Mitchell et al. teach cloning of the Arabidopsis thaliana FAH1 by designing PCR primers which are at least 80% identical with a sequence containing at least 10 consecutive nucleotides of the sequence of SEQ ID No. 5. Mitchell et al. teach amplification of the open reading frame from Arabidopsis thaliana for FAH1 (see PCR cloning

of an Arabidopsis thaliana homolog, page 28282 and figure 4, page 28285). Mitchell et al. teach isolating and sequencing the FAH1 gene, which encompasses nucleotides 240 bases upstream of the FAH1 gene which that would allow for the isolation of the promoter of the FAH gene (see figure 4, page 28285).

12. Claims 1-3, 5-6 are rejected under 35 U.S.C. 102(b) as being anticipated by as being anticipated by GenBank accession number AC003096 (gi 2598082, Nov. 7, 1997).

The GenBank accession number AC003096 teaches a nucleic acid sequence (positions 6867-7798) that comprises the sequence of instant SEQ ID No. 1. Therefore the sequence taught by GenBank accession number, AC003096 anticipates claims 1-3 and 5-6.

13. Claims 1-3 and 5 is rejected under 35 U.S.C. 102(b) as being anticipated by Brennan (US Patent 5474796, Dec. 1995).

With regards to claims 1-3, Brennan teaches an array having every possible permutation of a 3mer and a 10mer oligonucleotide (see example 4, column 9, lines 15-60, figure 1). Claim 5 is drawn to "a promoter sequence.... comprises a sequence having at least 80% identity with the sequence or a portion of the sequence" which is broadly interpreted to encompass any fragment of two or more nucleotides and can broadly encompasses any magnitude and/or content that comprise at least two nucleotides of SEQ ID No 1 or any promoter of any Arabidopsis FAH gene, which is anticipated by Brennan.

This rejection can be overcome by reciting "an isolated and purified nucleic acid molecule comprising the sequence of SEQ ID No 1".

Conclusion

No claims are allowable.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Sarae Bausch whose telephone number is (571) 272-2912. The examiner can normally be reached on M-F 10am-7pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Jones can be reached on (571) 272-0745. The fax phone number for the organization where this application or proceeding is assigned is (571) 273-8300.

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